1
SEQUENCE LISTING

<110>   SmithKline Beecham Corporation
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        Wisely , Bruce
        Collins, Jon

<120>   CAR LIGAND-BINDING DOMAIN POLYPEPTIDE CO-CRYSTALLIZED WITH A
        LIGAND, AND METHODS OF DESIGNING LIGANDS THAT MODULATE CAR
        ACTIVITY

<130>   PR60235

<150>   60/488,415
<151>   2003-07-18

<160>   7

<170>   PatentIn version 3.2

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<212>   DNA
<213>   Homo sapiens

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<221>   CDS
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tccaatcact ggcaactcct gagatcagag gaaaaccagc aacagcgtgg gagtttgggg   180

agaggcattc cataccagat tctgtggcct gcaggtgaca tgctgcctaa gagaagcagg   240

agtctgtgac agccacccca acacgtgacg tc atg gcc agt agg gaa gat gag   293
                                       Met Ala Ser Arg Glu Asp Glu
                                       1   5

ctg agg aac tgt gtg gta tgt ggg gac caa gcc aca ggc tac cac ttt   341
Leu Arg Asn Cys Val Val Cys Gly Asp Gln Ala Thr Gly Tyr His Phe
        10   15   20

aat gcg ctg act tgt gag ggc tgc aag ggt ttc ttc agg aga aca gtc   389
Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Val
    25   30   35

agc aaa agc att ggt ccc acc tgc ccc ttt gct gga agc tgt gaa gtc   437
Ser Lys Ser Ile Gly Pro Thr Cys Pro Phe Ala Gly Ser Cys Glu Val
40   45   50   55

agc aag act cag agg cgc cac tgc cca gcc tgc agg ttg cag aag tgc   485
Ser Lys Thr Gln Arg Arg His Cys Pro Ala Cys Arg Leu Gln Lys Cys
                60   65   70

tta gat gct ggc atg agg aaa gac atg ata ctg tcg gca gaa gcc ctg   533
Leu Asp Ala Gly Met Arg Lys Asp Met Ile Leu Ser Ala Glu Ala Leu

                                    2
              75   80   85

gca ttg cgg cga gca aag cag gcc cag cgg cgg gca cag caa aca cct   581
Ala Leu Arg Arg Ala Lys Gln Ala Gln Arg Arg Ala Gln Gln Thr Pro
        90   95   100

gtg caa ctg agt aag gag caa gaa gag ctg atc cgg aca ctc ctg ggg   629
Val Gln Leu Ser Lys Glu Gln Glu Glu Leu Ile Arg Thr Leu Leu Gly
        105   110   115

gcc cac acc cgc cac atg ggc acc atg ttt gaa cag ttt gtg cag ttt   677
Ala His Thr Arg His Met Gly Thr Met Phe Glu Gln Phe Val Gln Phe
120   125   130   135

agg cct cca gct cat ctg ttc atc cat cac cag ccc ttg ccc acc ctg   725
Arg Pro Pro Ala His Leu Phe Ile His His Gln Pro Leu Pro Thr Leu
                140   145   150

gcc cct gtg ctg cct ctg gtc aca cac ttc gca gac atc aac act ttc   773
Ala Pro Val Leu Pro Leu Val Thr His Phe Ala Asp Ile Asn Thr Phe
                155   160   165

atg gta ctg caa gtc atc aag ttt act aag gac ctg ccc gtc ttc cgt   821
Met Val Leu Gln Val Ile Lys Phe Thr Lys Asp Leu Pro Val Phe Arg
                170   175   180

tcc ctg ccc att gaa gac cag atc tcc ctt ctc aag gga gca gct gtg   869
Ser Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly Ala Ala Val
        185   190   195

gaa atc tgt cac atc gta ctc aat acc act ttc tgt ctc caa aca caa   917
Glu Ile Cys His Ile Val Leu Asn Thr Thr Phe Cys Leu Gln Thr Gln
200   205   210   215

aac ttc ctc tgc ggg cct ctt cgc tac aca att gaa gat gga gcc cgt   965
Asn Phe Leu Cys Gly Pro Leu Arg Tyr Thr Ile Glu Asp Gly Ala Arg
                220   225   230

gtg ggg ttc cag gta gag ttt ttg gag ttg ctc ttt cac ttc cat gga   1013
Val Gly Phe Gln Val Glu Phe Leu Glu Leu Leu Phe His Phe His Gly
                235   240   245

aca cta cga aaa ctg cag ctc caa gag cct gag tat gtg ctc ttg gct   1061
Thr Leu Arg Lys Leu Gln Leu Gln Glu Pro Glu Tyr Val Leu Leu Ala
                250   255   260

gcc atg gcc ctc ttc tct cct gac cga cct gga gtt acc cag aga gat   1109
Ala Met Ala Leu Phe Ser Pro Asp Arg Pro Gly Val Thr Gln Arg Asp
                265   270   275

gag att gat cag ctg caa gag gag atg gca ctg act ctg caa agc tac   1157
Glu Ile Asp Gln Leu Gln Glu Glu Met Ala Leu Thr Leu Gln Ser Tyr
280   285   290   295

atc aag ggc cag cag cga agg ccc cgg gat cgg ttt ctg tat gcg aag   1205
Ile Lys Gly Gln Gln Arg Arg Pro Arg Asp Arg Phe Leu Tyr Ala Lys
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ttg cta ggc ctg ctg gct gag ctc cgg agc att aat gag gcc tac ggg   1253
Leu Leu Gly Leu Leu Ala Glu Leu Arg Ser Ile Asn Glu Ala Tyr Gly
                315   320   325

3

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Tyr Gln Ile Gln His Ile Gln Gly Leu Ser Ala Met Met Pro Leu Leu
        330                 335                 340

cag gag atc tgc agc tgaggccatg ctcacttcct tccccagctc acctggaaca      1356
Gln Glu Ile Cys Ser
        345

ccctggatac actggagtgg gaaaatgctg ggaccaaaga ttgggccggg ttcaaaggga    1416

gcccagtggt tgcaatgaaa gactaaagca aaac                                1450
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<213>  Homo sapiens

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Gly Phe Phe Arg Arg Thr Val Ser Lys Ser Ile Gly Pro Thr Cys Pro
        35                  40                  45


Phe Ala Gly Ser Cys Glu Val Ser Lys Thr Gln Arg Arg His Cys Pro
    50                  55                  60


Ala Cys Arg Leu Gln Lys Cys Leu Asp Ala Gly Met Arg Lys Asp Met
65                  70                  75                  80


Ile Leu Ser Ala Glu Ala Leu Ala Leu Arg Arg Ala Lys Gln Ala Gln
                85                  90                  95


Arg Arg Ala Gln Gln Thr Pro Val Gln Leu Ser Lys Glu Gln Glu Glu
                100                 105                 110


Leu Ile Arg Thr Leu Leu Gly Ala His Thr Arg His Met Gly Thr Met
            115                 120                 125


Phe Glu Gln Phe Val Gln Phe Arg Pro Pro Ala His Leu Phe Ile His
        130                 135                 140


His Gln Pro Leu Pro Thr Leu Ala Pro Val Leu Pro Leu Val Thr His
145                 150                 155                 160


Phe Ala Asp Ile Asn Thr Phe Met Val Leu Gln Val Ile Lys Phe Thr
                165                 170                 175
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4

Lys Asp Leu Pro Val Phe Arg Ser Leu Pro Ile Glu Asp Gln Ile Ser
            180   185   190

Leu Leu Lys Gly Ala Ala Val Glu Ile Cys His Ile Val Leu Asn Thr
            195   200   205

Thr Phe Cys Leu Gln Thr Gln Asn Phe Leu Cys Gly Pro Leu Arg Tyr
    210   215   220

Thr Ile Glu Asp Gly Ala Arg Val Gly Phe Gln Val Glu Phe Leu Glu
225   230   235   240

Leu Leu Phe His Phe His Gly Thr Leu Arg Lys Leu Gln Leu Gln Glu
                245   250   255

Pro Glu Tyr Val Leu Leu Ala Ala Met Ala Leu Phe Ser Pro Asp Arg
            260   265   270

Pro Gly Val Thr Gln Arg Asp Glu Ile Asp Gln Leu Gln Glu Glu Met
            275   280   285

Ala Leu Thr Leu Gln Ser Tyr Ile Lys Gly Gln Gln Arg Arg Pro Arg
    290   295   300

Asp Arg Phe Leu Tyr Ala Lys Leu Leu Gly Leu Leu Ala Glu Leu Arg
305   310   315   320

Ser Ile Asn Glu Ala Tyr Gly Tyr Gln Ile Gln His Ile Gln Gly Leu
                325   330   335

Ser Ala Met Met Pro Leu Leu Gln Glu Ile Cys Ser
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ggg gcc cac acc cgc cac atg ggc acc atg ttt gaa cag ttt gtg cag   96

5

Gly Ala His Thr Arg His Met Gly Thr Met Phe Glu Gln Phe Val Gln
            20   25   30

ttt agg cct cca gct cat ctg ttc atc cat cac cag ccc ttg ccc acc   144
Phe Arg Pro Pro Ala His Leu Phe Ile His His Gln Pro Leu Pro Thr
        35   40   45

ctg gcc cct gtg ctg cct ctg gtc aca cac ttc gca gac atc aac act   192
Leu Ala Pro Val Leu Pro Leu Val Thr His Phe Ala Asp Ile Asn Thr
        50   55   60

ttc atg gta ctg caa gtc atc aag ttt act aag gac ctg ccc gtc ttc   240
Phe Met Val Leu Gln Val Ile Lys Phe Thr Lys Asp Leu Pro Val Phe
65   70   75   80

cgt tcc ctg ccc att gaa gac cag atc tcc ctt ctc aag gga gca gct   288
Arg Ser Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly Ala Ala
                85   90   95

gtg gaa atc tgt cac atc gta ctc aat acc act ttc tgt ctc caa aca   336
Val Glu Ile Cys His Ile Val Leu Asn Thr Thr Phe Cys Leu Gln Thr
            100   105   110

caa aac ttc ctc tgc ggg cct ctt cgc tac aca att gaa gat gga gcc   384
Gln Asn Phe Leu Cys Gly Pro Leu Arg Tyr Thr Ile Glu Asp Gly Ala
            115   120   125

cgt gtg ggg ttc cag gta gag ttt ttg gag ttg ctc ttt cac ttc cat   432
Arg Val Gly Phe Gln Val Glu Phe Leu Glu Leu Leu Phe His Phe His
        130   135   140

gga aca cta cga aaa ctg cag ctc caa gag cct gag tat gtg ctc ttg   480
Gly Thr Leu Arg Lys Leu Gln Leu Gln Glu Pro Glu Tyr Val Leu Leu
145   150   155   160

gct gcc atg gcc ctc ttc tct cct gac cga cct gga gtt acc cag aga   528
Ala Ala Met Ala Leu Phe Ser Pro Asp Arg Pro Gly Val Thr Gln Arg
                165   170   175

gat gag att gat cag ctg caa gag gag atg gca ctg act ctg caa agc   576
Asp Glu Ile Asp Gln Leu Gln Glu Glu Met Ala Leu Thr Leu Gln Ser
            180   185   190

tac atc aag ggc cag cag cga agg ccc cgg gat cgg ttt ctg tat gcg   624
Tyr Ile Lys Gly Gln Gln Arg Arg Pro Arg Asp Arg Phe Leu Tyr Ala
            195   200   205

aag ttg cta ggc ctg ctg gct gag ctc cgg agc att aat gag gcc tac   672
Lys Leu Leu Gly Leu Leu Ala Glu Leu Arg Ser Ile Asn Glu Ala Tyr
210   215   220

ggg tac caa atc cag cac atc cag ggc ctg tct gcc atg atg   714
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Phe Arg Pro Pro Ala His Leu Phe Ile His His Gln Pro Leu Pro Thr
        35   40   45

Leu Ala Pro Val Leu Pro Leu Val Thr His Phe Ala Asp Ile Asn Thr
    50   55   60

Phe Met Val Leu Gln Val Ile Lys Phe Thr Lys Asp Leu Pro Val Phe
65   70   75   80

Arg Ser Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly Ala Ala
            85   90   95

Val Glu Ile Cys His Ile Val Leu Asn Thr Thr Phe Cys Leu Gln Thr
            100   105   110

Gln Asn Phe Leu Cys Gly Pro Leu Arg Tyr Thr Ile Glu Asp Gly Ala
        115   120   125

Arg Val Gly Phe Gln Val Glu Phe Leu Glu Leu Leu Phe His Phe His
    130   135   140

Gly Thr Leu Arg Lys Leu Gln Leu Gln Glu Pro Glu Tyr Val Leu Leu
145   150   155   160

Ala Ala Met Ala Leu Phe Ser Pro Asp Arg Pro Gly Val Thr Gln Arg
            165   170   175

Asp Glu Ile Asp Gln Leu Gln Glu Glu Met Ala Leu Thr Leu Gln Ser
        180   185   190

Tyr Ile Lys Gly Gln Gln Arg Arg Pro Arg Asp Arg Phe Leu Tyr Ala
        195   200   205

Lys Leu Leu Gly Leu Leu Ala Glu Leu Arg Ser Ile Asn Glu Ala Tyr
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Gly Tyr Gln Ile Gln His Ile Gln Gly Leu Ser Ala Met Met
225   230   235

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<213>   Artificial

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<223>   Forward primer for amplifying amino acids 103-348, including
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aaggagcaa                                                             69


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<212>   DNA
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